

# SEQUENCE LISTING

<110> Georgopoulos, Katia  
Mogan, Bruce A.  
Kelly, Clair

<120> THE HELIOS GENE

<130> 10287/043001

<150> US 60/076,325

<151> 1998-02-27

<160> 17

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (1)...(1578)

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Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser	
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acg ccc aat gga cag cac gcc tcg cca agt cac atg aca agc aca aat	144
Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn	
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tct gta aag ctg gaa atg cag agt gat gaa gag tgt gac agg cag ccc	192
Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro	
50 55 60	
ctg agc cgt gag gat gag atc agg ggc cac gat gag ggg agc agc cta	240
Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu	
65 70 75 80	
gaa gaa ccc cta att gag agc agc gag gtg gcc gac aac agg aaa gtc	288
Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val	
85 90 95	
cag gac ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt aaa ctg	336
Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu	
100 105 110	
aaa tgt gac gtc tgt ggc atg gtt tgc att ggg ccc aat gtg ctt atg	384
Lys Cys Asp Val Cys Gly Met Val Cys Ile Gly Pro Asn Val Leu Met	
115 120 125	

gta cat aaa agg agt cac act ggt gag cgg ccc ttc cac tgt aac cag	432
Val His Lys Arg Ser His Thr Gly Glu Arg Pro Phe His Cys Asn Gln	
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Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys	
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Leu His Ser Gly Glu Lys Pro Phe Lys Cys Pro Phe Cys Ser Tyr Ala	
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Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val	
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Gly Lys Pro His Lys Cys Asn Tyr Cys Gly Arg Ser Tyr Lys Gln Arg	
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acg tca ctg gag gaa cac aag gaa cgc tgt cac aac tat ctc cag aat	672
Thr Ser Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Gln Asn	
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245 250 255	
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260 265 270	
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Leu Met Arg Phe Ser Tyr Pro Asp Ile His Phe Asp Met Asn Leu Thr	
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Tyr Glu Lys Glu Ala Glu Leu Met Gln Ser His Met Met Asp Gln Ala	
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Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His Pro Leu	
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Met Gln His Ala Pro Ser Thr Ile Ala Glu Val Ala Pro Val Ile Ser	
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Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg Pro Ile	
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gaa Glu	ttt Phe	tca Ser 515	tca Ser	cac His	att Ile	gtt Val	ggg Gly 520	ggg Gly	cag Gln	cac His	aca Thr	ttc Phe 525	cac His			1578
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Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser  
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 Glu Ser Ser His Asp Asp Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu  
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 Asn Pro Lys Arg Lys Gln Ser Pro Ala Tyr Met Lys Glu Asp Val Lys  
 405 410 415  
 Ala Leu Asp Ala Thr Lys Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr  
 420 425 430  
 Lys Val Phe Asn Gly Glu Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu  
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 His Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met  
 450 455 460  
 Gly Cys His Gly Tyr Arg Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr  
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 cgacagagct ggaaatggtg atgaatcttt ttttaacaaa ggacaatttc ttttcattgc 180  
 actttgact atg gaa aca gag gct att gat ggc tat ata acg tgt gac aat 231  
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 gag ctt tca ccc gaa agg gag cac tcc aat atg gca att gac ctc acc 279  
 Glu Leu Ser Pro Glu Arg Glu His Ser Asn Met Ala Ile Asp Leu Thr 30  
 15 20 25  
 tca agc aca ccc aat gga cag cat gcc tca cca agt cac atg aca agc 327  
 Ser Ser Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser 45  
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 aca gat tca gta aag cta gaa atg cag agt gat gaa gag tgt gac agg 375  
 Thr Asp Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg 60  
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 Lys Pro Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser 75  
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 Ser Leu Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg 90  
 80 85 90  
 gaa gtc cag gag ctt caa ggc gag gga gga atc cgg ctt ccg aat ggt 519  
 Glu Val Gln Glu Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly 110  
 95 100 105



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caa gcc atc aac aat gca atc acc tac ctt gga gct gag gcc ctt cac Gln Ala Ile Asn Asn Ala Ile Thr Tyr Leu Gly Ala Glu Ala Leu His 320 325 330	1191
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Pro Ile Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala	
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415 420 425 430	
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Gly Glu Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val	
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Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly	
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Arg Tyr Glu Phe Ser Ser His Ile Val Arg Gly Glu His Thr Phe His	
515 520 525	
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cacttacaat cccacctttc ctcaaattgt gtacctttta tttttttaat ataatactgg	1887
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 <213> Homo sapiens

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 Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Lys Pro  
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Lys	Cys	Asp	Val	Cys	Gly	Met	Val	Cys	Ile	Gly	Pro	Asn	Val	Leu	Met
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Ser	Asn	Ser	Cys	Leu	Asp	Ser	Thr	Asp	Ser	Glu	Ser	Ser	His	Asp	Asp
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His	Gln	Ser	Tyr	Gln	Gly	His	Pro	Ala	Leu	Asn	Pro	Lys	Arg	Lys	Gln
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Leu	Asp	His	Val	Met	Tyr	Thr	Ile	His	Met	Gly	Cys	His	Gly	Tyr	Arg
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Asp	Pro	Leu	Glu	Cys	Asn	Ile	Cys	Gly	Tyr	Arg	Ser	Gln	Asp	Arg	Tyr
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Glu	Phe	Ser	Ser	His	Ile	Val	Arg	Gly	Glu	His	Thr	Phe	His		
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1. The first step is to identify the problem. This involves understanding the current situation and what needs to be changed.

-12-

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 Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly Tyr His  
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<210> 8  
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 Lys Pro His Glu Ile Glu Asn Val Asp Ser Arg Glu Ala Pro Ala Asn  
 35 40 45  
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 Ser Asp Arg Asp Glu Asn Ile Met Lys Pro Glu Pro Met Gly Asp Ala  
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 Glu Glu Ser Glu Met Pro Tyr Ser Tyr Ala Arg Glu Tyr Ser Asp Tyr  
 85 90 95  
 Glu Ser Ile Lys Leu Glu Arg His Val Pro Tyr Asp Asn Ser Arg Pro  
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 Thr Ser Gly Lys Met Asn Cys Asp Val Cys Gly Leu Ser Cys Ile Ser  
 115 120 125  
 Phe Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro  
 130 135 140  
 Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu  
 145 150 155 160  
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 Arg Thr His Ser Val Glu Lys Pro Tyr Lys Cys Glu Phe Cys Gly Arg  
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